

SCORE Search Results Details for Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_083145_us-10-552-515-1.rag.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 24, 2008, 08:32:16 ; Search time 263 Seconds
(without alignments)
2135.186 Million cell updates/sec

Title: US-10-552-515-1
Perfect score: 4950
Sequence: 1 MRMAATAWAGLQGFPPLPTLC.....SELSSHWTPTFTVPKASQLQQ 933

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
 10: geneseqp2005:*
 11: geneseqp2006:*
 12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4950	100.0	933	8	ADT77664	Adt77664 Splice va
2	4950	100.0	933	11	AEL84788	Ael84788 Tumor mar
3	4531.5	91.5	885	10	AEB13426	Aeb13426 Human pro
4	4364.5	88.2	843	10	AEB13424	Aeb13424 Human pro
5	3736	75.5	898	4	ABG15488	Abg15488 Novel hum
6	1531.5	30.9	920	6	ADB64420	Adb64420 Human pro
7	1511.5	30.5	920	6	ABP58666	Abp58666 Human dih
8	1504	30.4	981	8	ADK52114	Adk52114 Human ato
9	1504	30.4	981	12	AEN06206	Aen06206 Human eso
10	1489	30.1	1017	12	AFB77190	Afb77190 Mouse TM-
11	1488	30.1	960	11	AEG11142	Aeg11142 Human tra
12	1479.5	29.9	840	11	AEG11146	Aeg11146 Human tra
13	1464	29.6	1003	7	ADG48280	Adg48280 Human ret
14	1455	29.4	913	11	AEH82071	Aeh82071 Human gna
15	1445	29.2	1219	4	ABB62812	Abb62812 Drosophil
16	1445	29.2	1219	10	AFB95185	Afb95185 Fruit fly
17	1402.5	28.3	910	6	ADC42854	Adc42854 REMAP pro
18	1402.5	28.3	910	11	AEL84658	Ael84658 Tumor mar
19	1369.5	27.7	1075	4	ABB65993	Abb65993 Drosophil
20	1369.5	27.7	1075	10	AFC04729	Afc04729 Fruit fly
21	1367.5	27.6	712	11	AEG11145	Aeg11145 Human tra
22	1199.5	24.2	1058	4	ABB65022	Abb65022 Drosophil
23	1199.5	24.2	1058	10	AFC01816	Afc01816 Fruit fly
24	1154	23.3	596	6	ADB64387	Adb64387 Human pro
25	1061.5	21.4	594	4	AAB92637	Aab92637 Human pro
26	1061.5	21.4	594	5	ABP43811	Abp43811 FLJ10261
27	1061.5	21.4	594	8	ADJ75429	Adj75429 Marker ge
28	1061.5	21.4	594	8	ADN04848	Adn04848 Antipsori
29	1061.5	21.4	594	11	AEG11143	Aeg11143 Human FLJ
30	1037.5	21.0	782	6	ADX42387	Adx42387 Human col
31	1037.5	21.0	782	7	ADT95905	Adt95905 Colon can
32	1037.5	21.0	782	8	ADQ96288	Adq96288 T cell ac
33	1037.5	21.0	782	8	ADQ96104	Adq96104 T cell ac
34	912.5	18.4	475	6	ADB64962	Adb64962 Human pro
35	905	18.3	642	7	ADM05798	Adm05798 Human pro

36	905	18.3	642	10	AEC88728	Aec88728 Human cDN
37	905	18.3	642	11	AEG11144	Aeg11144 Human FLJ
38	819.5	16.6	443	5	ABP41785	Abp41785 Human ova
39	817.5	16.5	179	6	AAO29613	Aao29613 Human Nov
40	784.5	15.8	390	5	ABB90382	Abb90382 Human pol
41	735	14.8	139	5	AAE24066	Aae24066 Human pro
42	722.5	14.6	360	4	AAM40391	Aam40391 Human pol
43	711.5	14.4	346	8	ADP29628	Adp29628 Human sec
44	695.5	14.1	608	8	ADQ96298	Adq96298 T cell ac
45	695.5	14.1	608	8	ADQ96286	Adq96286 T cell ac

ALIGNMENTS

RESULT 1

ADT77664

ID ADT77664 standard; protein; 933 AA.

XX

AC ADT77664;

XX

DT 15-JUN-2007 (revised)

DT 13-JAN-2005 (first entry)

XX

DE Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.

XX

KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;
 KW prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;
 KW NGEP long variant; NGEP long variant [Homo sapiens]; G05886.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .345

FT /label= Cytoplasmic

FT Region 157. .933

FT /note= "An immunogenic fragment comprising 8 consecutive
 FT amino acids that specifically binds to an antibody that
 FT specifically binds to a polypeptide comprising amino
 FT acids 157-933 is referred to in Claim 1"

FT Region 170. .178

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 215. .223

FT /note= "Epitope, predicted to bind HLA2-01"

FT Region 258. .266

FT /note= "Epitope, predicted to bind HLA2-01"

FT Domain 346. .368

FT /label= Transmembrane

FT Domain 369. .421

FT		/label= External
FT		/note= "Cell surface"
FT	Region	403. .411
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	422. .441
FT		/label= Transmembrane
FT	Region	427. .435
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	442. .501
FT		/label= Cytoplasmic
FT	Domain	502. .524
FT		/label= Transmembrane
FT	Domain	525. .543
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	544. .566
FT		/label= Transmembrane
FT	Region	557. .565
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Region	562. .570
FT		/note= "Epitope, predicted to bind HLA2-01"
FT	Domain	567. .586
FT		/label= Cytoplasmic
FT	Domain	587. .609
FT		/label= Transmembrane
FT	Domain	610. .714
FT		/label= External
FT		/note= "Cell surface"
FT	Domain	715. .737
FT		/label= Transmembrane
FT	Domain	738. .761
FT		/label= Cytoplasmic
FT	Domain	762. .784
FT		/label= Transmembrane
FT	Domain	785. .933
FT		/label= External
FT		/note= "Cell surface"
FT	Region	846. .854
FT		/note= "Epitope, predicted to bind HLA2-01"

XX

PN WO2004092213-A1.

XX

PD 28-OCT-2004.

XX

PF 05-APR-2004; 2004WO-US010588.

XX

PR 08-APR-2003; 2003US-0461399P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Pastan I, Bera TK, Lee B;
 XX
 DR WPI; 2004-758338/74.
 DR N-PSDB; ADT77665.
 DR PC:NCBI; gi48093524.
 XX
 PT New Splice Variant-*Novel Gene Expressed in Prostate polypeptide or*
 PT *encoding nucleic acid molecule for diagnosing, preventing or treating*
 PT *cancer, especially prostate cancer.*
 XX
 PS Claim 1; SEQ ID NO 1; 88pp; English.
 XX
 CC The present sequence is the protein sequence of splice variant-novel gene
 CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
 CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
 CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
 CC a prostate sample. Claimed methods for detecting prostate cancer in a
 CC subject comprise: contacting the sample with an antibody that
 CC specifically binds a SV-NGEP polypeptide and detecting the formation of
 CC an immune complex; or detecting an increase in expression of SV-NGEP
 CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
 CC detect metastatic prostate cancer cells at locations other than the
 CC prostate. A claimed method for producing an immune response against a
 CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
 CC comprises administering the polypeptide, or a polynucleotide encoding it,
 CC to produce an immune response that decreases growth of the prostate
 CC cancer. A claimed method for inhibiting the growth of a malignant cell
 CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
 CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
 CC cell, and contacting the malignant cell with the activated CTLs.
 CC Alternatively, growth of a malignant cell is inhibited by contact with an
 CC antibody that specifically binds an SV-NGEP polypeptide, where the
 CC antibody is linked to an effector molecule (chemotherapeutic agent or
 CC toxin) that inhibits growth of the malignant cell. This may be performed
 CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
 CC sample are also claimed.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 933 AA;

Query Match 100.0%; Score 4950; DB 8; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAAHERWAMTSETSSGSHCARSRMLRRRA 60
 |||

Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEWAMTSETSSGSHCARSRMLRRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWWEEDL	120
Db	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWWEEDL	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVILLEVPDPPEYYSCRFRVNKLPRF	240
Db	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVILLEVPDPPEYYSCRFRVNKLPRF	240
Qy	241	LGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFFLHDGPFKT	300
Db	241	LGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFFLHDGPFKT	300
Qy	301	PPEGFQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	301	PPEGFQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Qy	421	GGTVFFSLFMALWAVLLLEYWKRSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLLEYWKRSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAW	540
Qy	541	ASRIASLTGSVNLVLFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQVNFY	600
Db	541	ASRIASLTGSVNLVLFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQVNFY	600
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Qy	661	LIPKLKGWQKFRLSRKKRKAGASAGSQGPWEDDYELVPCEGFLFDEYLEMVLQFGFVTI	720
Db	661	LIPKLKGWQKFRLSRKKRKAGASAGSQGPWEDDYELVPCEGFLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFAALLNNWEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFAALLNNWEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780

```

Qy      781 AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDDGHYS 840
      |||
Db      781 AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDDGHYS 840

Qy      841 QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVDPDIPESVEIKVKREYLLAKQALAENEVL 900
      |||
Db      841 QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVDPDIPESVEIKVKREYLLAKQALAENEVL 900

Qy      901 FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933
      |||
Db      901 FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933

```

RESULT 2

AEL84788

ID AEL84788 standard; protein; 933 AA.

XX

AC AEL84788;

XX

DT 18-OCT-2007 (revised)

DT 15-JUN-2007 (revised)

DT 28-DEC-2006 (first entry)

XX

DE Tumor marker gene NGEF SEQ ID NO 155.

XX

KW cytostatic; diagnosis; prognosis; tumor marker; gene expression;

KW drug screening; cancer; neoplasm; NGEF; BOND_PC; NGEF long variant;

KW G05886.

XX

OS Homo sapiens.

XX

PN W02006110593-A2.

XX

PD 19-OCT-2006.

XX

PF 07-APR-2006; 2006W0-US013172.

XX

PR 07-APR-2005; 2005US-0669342P.

PR 11-OCT-2005; 2005US-0725982P.

XX

PA (MACR-) MACROGENICS INC.

XX

PI Von Haller PD, Schummer M, Meyer DW, Schubert LA, Tjoelker LW;

XX

DR WPI; 2006-814687/82.

DR N-PSDB; AEL84787.

DR REFSEQ; NP_001001891.

DR PC:NCBI; gi48093524.

XX
PT Detecting or diagnosing cancer in a subject comprises determining
PT expression of at least one gene, and comparing level of expression to a
PT control sample from a normal subject, where increased expression level
PT indicates cancer.

XX
PS Claim 8; SEQ ID NO 155; 583pp; English.

XX
CC The invention describes a method of detecting or diagnosing cancer in a
CC subject comprising determining the expression level of at least one gene,
CC and comparing the level of expression to a corresponding control sample
CC from a normal subject, where cancer is detected or diagnosed if there is
CC an increase in the expression level of the gene relative to the
CC expression in the control sample. Also described are: identifying a
CC compound to be tested for its ability to prevent, treat, manage, or
CC ameliorate cancer or its symptom; a compound identified by the method;
CC treating cancer in a patient; treating a cancer in a subject that is
CC fully or partially refractory to a first treatment in a patient; and a
CC pharmaceutical composition comprising an amount of an antibody selected
CC from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2,
CC anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT,
CC anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2D1, anti-MGC2963, anti-
CC KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-
CC FLJ90709, anti-VZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-
CC C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-
CC SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB,
CC anti-XT3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-
CC PR01855, anti-C2orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-
CC FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-
CC IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti-FLJ11848, anti-ENTPD2, anti-
CC PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26,
CC anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2,
CC anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-
CC FLJ14681, anti-C2orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-
CC C2orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-
CC FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-
CC DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-
CC MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b
CC antibody, and a pharmaceutical carrier. The methods are useful for
CC detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary,
CC prostate, pancreas, or bladder cancer. This is the amino acid sequence of
CC NGEP, altered levels of expression are useful in the diagnosis or
CC prognosis of cancer.

CC
CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.

XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 4950; DB 11; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCARSRMLRRRA	60
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCARSRMLRRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAKPRIADFVLVWEEDL	120
Db	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAKPRIADFVLVWEEDL	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCFRVKNLPRF	240
Db	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCFRVKNLPRF	240
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLGLIQLLAEGVLSAAFLHDGPFKT	300
Db	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLGLIQLLAEGVLSAAFLHDGPFKT	300
Qy	301	PPEGFOAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	301	PPEGFOAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDDH	420
Db	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDDH	420
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGNTLLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGNTLLAAW	540
Qy	541	ASRIASLTGSVNVLFILILSKIYVSLAHVLTREWHRHTQTKFEDAFTLKVFIFQFVNFI	600
Db	541	ASRIASLTGSVNVLFILILSKIYVSLAHVLTREWHRHTQTKFEDAFTLKVFIFQFVNFI	600
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGLIELAQELLVIMVGKQVINNMQEV	660
Db	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGLIELAQELLVIMVGKQVINNMQEV	660
Qy	661	LIPKLKGWQKFRRLRSKRKAGASAGASQGPWEDDYELVPCEGFLFDEYLEMVLQFGFVTI	720

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Db      661  |||LIPKLKGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI 720
Qy      721  FVAACPLAPLPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWPHILAGLTHLAVISN 780
Db      721  |||FVAACPLAPLPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWPHILAGLTHLAVISN 780
Qy      781  AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCryRAFRDDDGHSY 840
Db      781  |||AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCryRAFRDDDGHSY 840
Qy      841  QTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVDPDIPESVEIKVKREYYLAKQALAENEVL 900
Db      841  |||QTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVDPDIPESVEIKVKREYYLAKQALAENEVL 900
Qy      901  FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933
Db      901  |||FGTNGTKDEQPKGSELSSHWTPFTVPKASQLQQ 933

```

RESULT 3

AEB13426

ID AEB13426 standard; protein; 885 AA.

XX

AC AEB13426;

XX

DT 22-SEP-2005 (first entry)

XX

DE Human prostate specific polypeptide #2.

XX

KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
 KW cancer; prostate tumor; cytostatic; neoplasm.

XX

OS Homo sapiens.

XX

PN W02005062788-A2.

XX

PD 14-JUL-2005.

XX

PF 16-DEC-2004; 2004WO-US042406.

XX

PR 22-DEC-2003; 2003US-0531809P.

XX

PA (AVAL-) AVALON PHARM INC.

XX

PI Weigle B, Ebner R;

XX

DR WPI; 2005-497793/50.

DR N-PSDB; AEB13425.

XX

PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.

XX
PS Claim 12; SEQ ID NO 5; 59pp; English.

XX

CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of
CC the invention.

XX
SQ Sequence 885 AA;

Query Match 91.5%; Score 4531.5; DB 10; Length 885;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 855; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy 1 MRMAATAWAGLQGPPPLTLCPAVRTGLYCRDQAHAEAWAMTSETSSGSHCARSMLRRA 60

Db 5 MRMAATAWAGLOGPPLPTLCPAVRTGLYCRDOAHAERWAMTSETSSGSHCA--RMLRRRA 62

Ov 61 OEDSTVLIDVSPPEAEKRGSYGSTAHASEPGG00AAACRAGSPAKPRIADFVLVWEEDL 120

Db 782 AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRYAFRDDDDGHYS 841

Qy 841 QTYWNLLAIRLAFVIVFE 858
 |||

Db 842 QTYWNLLAIRLAFVIVFE 859

RESULT 4

AEB13424

ID AEB13424 standard; protein; 843 AA.

XX

AC AEB13424;

XX

DT 22-SEP-2005 (first entry)

XX

DE Human prostate specific polypeptide #1.

XX

KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
 KW cancer; prostate tumor; cytostatic; neoplasm.

XX

OS Homo sapiens.

XX

PN WO2005062788-A2.

XX

PD 14-JUL-2005.

XX

PF 16-DEC-2004; 2004WO-US042406.

XX

PR 22-DEC-2003; 2003US-0531809P.

XX

PA (AVAL-) AVALON PHARM INC.

XX

PI Weigle B, Ebner R;

XX

DR WPI; 2005-497793/50.

DR N-PSDB; AEB13423.

XX

PT Novel isolated prostate specific polypeptide, useful for treating cancer,
 PT and identifying agent that modulates activity of cancer related gene.

XX

PS Claim 12; SEQ ID NO 3; 59pp; English.

XX

CC The invention relates to an isolated prostate specific polypeptide
 CC comprising one or more immunogenic fragments. The invention also relates
 CC to a method of identifying an agent that modulates the activity of a
 CC cancer related gene involving contacting a compound with a cell
 CC containing a gene under conditions promoting the expression of the gene,
 CC detecting a difference in expression of the gene relative to when the
 CC compound is not present and identifying an agent that modulates the

activity of a cancer related gene, a method of identifying an anti-neoplastic agent involving contacting a cell exhibiting neoplastic activity with a compound first identified as a cancer related gene modulator using and determining a decrease in neoplastic activity after contacting, when compared to when the contacting does not occur, or administering an agent first identified to an animal exhibiting a cancer condition and detecting a decrease in cancerous condition, a method of determining the cancerous status of a cell involving determining an increase in the level of expression in a cell of a gene where an elevated expression relative to a known non-cancerous cell indicates a cancerous state or potentially cancerous state, an antibody that reacts with a prostate specific polypeptide, an immunoconjugate comprising the antibody and a cytotoxic agent, a method of treating cancer involving contacting a cancerous cell in vivo with an agent having activity against a prostate specific polypeptide and an immunogenic composition the prostate specific polypeptide. The prostate specific polypeptide is useful for identifying an agent that modulates the activity of a cancer related gene. The immunogenic composition is useful for treating cancer, preferably prostate cancer in an animal, e.g. human, which involves administering the immunogenic composition that is sufficient to elicit the production of cytotoxic T lymphocytes specific for the prostate specific polypeptide. The invention is useful for identifying anti-neoplastic agents. This sequence represents a human prostate specific polypeptide of the invention.

Sequence 843 AA;

Query Match 88.2%; Score 4364.5; DB 10; Length 843;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 824; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy	1	MRMAATAWAGLQGPPLTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCARSRMLRRA	60
Db	5	MRMAATAWAGLQGPPLTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCA--RMLRRA	62
Qy	61	QEEDSTVLIDVSPPEAEKRGSGYSTAHASEPGGQQAACRAGSFAKPRIADFVLVWEEDL	120
Db	63	QEEDSTVLIDVSPPEAEKRGSGYSTAHASEPGGQQAACRAGSFAKPRI-DFVLVWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFDLNLAAGLCVDQQDVQDGNNTTVHYALLSASWAVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFDLNLAAGLCVDQQDVQDGNNTTVHYALLSASWAVLC	181
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLVVPDPPEYYSCRFVKNLPRF	240
Db	182	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLVVPDPPEYYSCRFVKNLPRF	241
Qy	241	LGSNDQDTFTTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFLPHDGPFTK	300

Db	242	LGSDNQDTFFTTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFLPHDGPFFT	301
Qy	301	PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVLYFAWLGFYTGWLLPA	360
Db	302	PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVLYFAWLGFYTGWLLPA	361
Qy	361	AVVGTLLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	362	AVVGTLLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAW	541
Qy	541	ASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFI	600
Db	542	ASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFI	601
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGQVINNMQEV	660
Db	602	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGQVINNMQEV	661
Qy	661	LIPKLKGWWQKFLRLRSKKRKAGASAGSQGPWEDDYELVPC EGLFDEYLEMVLQFGFVTI	720
Db	662	LIPKLKGWWQKFLRLRSKKRKAGASAGSQGPWEDDYELVPC EGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	722	FVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	781
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	827
Db	782	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	828

RESULT 5

ABG15488

ID ABG15488 standard; protein; 898 AA.

XX

AC ABG15488;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #15479.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS79675.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 45847; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 898 AA;

Query Match 75.5%; Score 3736; DB 4; Length 898;
 Best Local Similarity 82.3%; Pred. No. 0;
 Matches 727; Conservative 4; Mismatches 16; Indels 136; Gaps 6;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAE-----	37
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEATDVVLLAPFCQPKTRSHGTCPP	60
Qy	38	-----W---AMTSETS-----SG	47
		:	
Db	61	TERDPRGEGSTEYPRGRVDGIQGWGTRALTGWTDRLRLCQACQTLPPRHWFPLPGARGWLGG	120
Qy	48	SHCA-----RSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	87
		:	
Db	121	SPCAHQESLPSQSPILLRVESVKSRLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	180
Qy	88	ASEPGGQQAACRAGSPAKPRIADFVLVWEEDLKLDQQDSAARDRTDMHRTWRETFLDN	147
Db	181	ASEPGGQQAACRAGSPAKPRIADFVLVWEEDLKLDQQDSAARDRTDMHRTWRETFLDN	240
Qy	148	LRAAGLCVDQDQDGNNTTVHYALLSASWAVLCYYAEDRLKLPLQELPNQASNWSAGLL	207
Db	241	LRAAGLCVDQDQDGNNTTVHYALLSASWAVLCYYAEDRLKLPLQDYPTRPPTGRPACC	300
Qy	208	AWLGIPNVLLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	267
Db	301	AWLGIPNVLLLEVVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	360
Qy	268	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN	327
Db	361	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN	420
Qy	328	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	387
Db	421	KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	480
Qy	388	KDSFEMCPLCLDCPFWLLSSACALAQ----AGRLFDHGGTVFFSLFMALWAVLLLEYWKR	443
Db	481	KDSFEMCPLCLDCPFWLLSSACALAQVREEAGRLFDHGGTVFFSLFMALWAVLLLEYWKR	540
Qy	444	KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARMLAGSVV	503
Db	541	KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARMLAGSVV	600
Qy	504	IVVMVAVVMCLVSIILYRAIMAIIVSRSGNTLLAAWASRIASLTGSVVNLVFLILISKI	563

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Db      601  IVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSAVVNLVFIILLSKI  660
Qy      564  YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTL  623
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTL  720
Qy      624  FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLSRKKRKA  683
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLSRKKRKA  780
Qy      684  SAGASQGPWEDDYELVPCGLFDEYLEM-----  711
        |||||||||||||||||||||||||||
Db      781  SAGASQGPWEDDYELVPCGLFDEYLEMGAGFCPNACPELVPELTEPEKARDQPEARSAG  840
Qy      712  -----VLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKE  747
        |||||||||||||||||||||||||||
Db      841  QDSRPEAVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKE  883

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RESULT 6

ADB64420

ID ADB64420 standard; protein; 920 AA.

XX

AC ADB64420;

XX

DT 15-JUN-2007 (revised)

DT 04-DEC-2003 (first entry)

XX

DE Human protein encoded by clone FEBRA20031280.

XX

KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour; BOND_PC; transmembrane protein 16D;
 KW transmembrane protein 16D (eight membrane-spanning domains);
 KW transmembrane protein 16D [Homo sapiens]; TMEM16D; FLJ34221; FLJ34272;
 KW FLJ35277; MGC130026; unnamed protein product;
 KW unnamed protein product [Homo sapiens].

XX

OS Homo sapiens.

XX

PN EP1308459-A2.

XX

PD 07-MAY-2003.

XX

PF 28-MAR-2002; 2002EP-00007401.

XX

PR 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-0350978P.

XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-450961/43.
 DR N-PSDB; ADB62450.
 DR PC:NCBI; gi30520318.
 XX
 PT New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 PS Claim 1; Page; 222pp; English.
 XX
 CC The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 920 AA;

Query Match 30.9%; Score 1531.5; DB 6; Length 920;

Best Local Similarity 37.9%; Pred. No. 1.1e-147;

Matches 360; Conservative 168; Mismatches 316; Indels 105; Gaps 29;

Qy	44	TSSGSHCARSMRLRRRAQEEDSTVLID---VSPPEAE-----KRGSYGST---AHASEP	91
		: ::: : : : :	
Db	4	SSSGITNGKTKVFPVA--KDVNILEFDELEAVSSPCKDDDSLHPGNLTSTSDASRLEA	61
Qy	92	GGQQAACRAGS-----PAKPRIADFLVWVEEDLKLDRQQDSDAARDRTDMHRTWRETFD	146
		: : : :: : : : :	
Db	62	GGETVPERNKSNGLYFRDGKCRIDYILVYR-----SNPQTEK---REVFER	105
Qy	147	NLRAAGLCVDQDQDGNNTTVHYALLSASWAVLCYYAEDLRLKLPQE---LPNQASNW	202
		: ::: : : : : : : :	
Db	106	NIRAEGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRKRIYYLPRRYKFM	164
Qy	203	S-----AGLLAWLGIPNVLL--EVVPDVP- EYYSRFRVNKLPRFLGSDNQDTFFTST	253
		: : : : : : : : : : :	
Db	165	SRIDKQISRLRRWLPPKPMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA	223
Qy	254	KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQR	313
		: : : : : : : : : : : : :	
Db	224	TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHR	282
Qy	314	QVLFQHWARWGKWNKYQPLDHVRRYFGEKVYFAWLGFYTGWLLPAAVVGTLVFLVGC	373
		::: :	
Db	283	HLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMFLFPAF IGLFVFLYGV	342
Qy	374	LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSFLFMA	432
		: ::: : :	
Db	343	TLDHSQVSKVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFFAVFM	401
Qy	433	WAVLLELYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER	491
		: : : : :	
Db	402	WATVLEFWKRRRAVIAYDWDLDWEEEEIEIRPQFEAKYSKKERMNPISGKPEPYQFT	461
Qy	492	SRARRLAGSVVIVVMVAVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIA	545
		: :: : : : : : : : : : :	
Db	462	DKCSRLIVSASGIFFMICVIAAVFGIVYRVTV-----STFAAFKQALIRNNSQVA	514
Qy	546	SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTQKFEDAFTLKVFIFQVFNFYSSP	603
		: : ::: : : : ::: :	
Db	515	T-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLQFVNLSST	573
Qy	604	VYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELIVIMVGKQVINNMQEVLI	662
		: : : :	
Db	574	FYIAFFLGRFTGHPGAYLRRLNRWRLEECHPSGCLIDLQMGMIMVLKQTNWNNFMELGY	633
Qy	663	PKLKGWWQKFLRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI	720
		: : : : :	

Db 634 PLIQNWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI 690

Qy 721 FVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWPHILAGLTHLAVISN 780
 ||| ||| ||| :||| ||| ::|||:| ||:||||: || |: |:|:|

Db 691 FVAAFPLAPLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITN 750

Qy 781 AFLLAFSSDFLPRAYRW-----TRAHDLRGFLNFTLA-----RAP 816
 ||:| :||:| | : : |:| :|:

Db 751 AFVIAITSDFIPLRVYAYKYGPCAGQGEAGQKCMVGYNASLSVFRISDFENRSEPESEDG 810

Qy 817 SSFAAAHNRTCRYRAFRDDDGH----YSQTYWNLLAIRLAFVIVFEHVSVGRLLDLL 871
 | |: : ||| :| | : :||:| |||:||||:| | : |: |

Db 811 SEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFWHVLAAFLAFIIVFEHLVFCIKHLISYL 870

Qy 872 VPDIPESVEIKVKREYLLAKQALAENEVLFGTNGTKDEQPKGSELSSH 920
 :||:|: : ::|| || :: : | |: |: : | : |

Db 871 IPDLFKDLDRMRREKYLQEMMYEAELERLQKERKERKKNGKAHHNEW 919

RESULT 7

ABP58666

ID ABP58666 standard; protein; 920 AA.

XX

AC ABP58666;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human dihydropyrimidinase related protein 1-101.20.

XX

KW Human; dihydropyrimidinase related protein 1-101.20;

KW recombinant production; gene therapy; psychosis; development disorder;

KW uracil-related metabolic disorder; thymine-related metabolic disorder;

KW pyrimidine metabolic disorder.

XX

OS Homo sapiens.

XX

PN CN1364894-A.

XX

PD 21-AUG-2002.

XX

PF 10-JAN-2001; 2001CN-00105195.

XX

PR 10-JAN-2001; 2001CN-00105195.

XX

PA (BIO-W) BIOWINDOW GENE DEV INC SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2003-000532/01.

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4 083145 us-10-552-515-1.rag&ItemType=4&startByte=0 (22 of 44)10/10/2008 8:48:10 AM

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      :      ::|:| : |   ||:|   || | : | :|   ||:|   |||::|::|:
Db      343  TLDHSQVSKVEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAV 401

Qy      433  WAVLLELYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER 491
      || : ||:|::| : ||:| ||   ||:| ||   |||:| :   :   |||:|: ||
Db      402  WATVFLEFWKRRRAVIAYDWDLDWEEEEEEIIRPQFEAKYSKKERMNPISGKPEPYQAF 461

Qy      492  SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVSRSGNTLLA-AWA-----SRIA 545
      :   :: :   |   ||:| :   :   ||:| :   :   :   |   |   ||   ||:|
Db      462  DKCSRLIVSASGIFFMICVVIAAVFGIVYIRVVTV-----STFAAFKVALIRNNSQVA 514

Qy      546  SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSP 603
      : ||:| :   |   ||:|: ||   ||:| ||   |||::|:|:|:|:|:|:|:| ||
Db      515  T-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLQFVNLSNST 573

Qy      604  VYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLI 662
      ||||| ||| ||:| ||   |   |||   |||:|:|:|:|:|:|:| ||   ||
Db      574  FYIAFFLGRFTGHPGAYLRLINRWLEECHPSGLIDLQMGIIMVLKQTWNNFMELGY 633

Qy      663  PKLKGWWQKFLRLSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI 720
      | : || :   |   :::|   |   || || ||   ||:|:|:|:|:|:| ||
Db      634  PLIQNWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLYDEYLEMILQFGFTTI 690

Qy      721  FVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN 780
      |||| | |||| | |||| : |||| | || : ||:|:|   ||:|:| : || | : | :|:|
Db      691  FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIGYGILEGIGILSVITN 750

Qy      781  AFLFLAFSSDFLPRAYYRW-----TRAHDLRGFLNFTLA-----RAP 816
      ||:|:| : ||:|:|   | :   :   ||:|:| : ||
Db      751  AFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDG 810

Qy      817  SSFAAAHNRTCRYRAFRRDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLL 871
      | : :   : |||| : ||   | : : ||:| |||:|:|:|:|:| : | : |
Db      811  SEFSGTPLKYCRYRDRDPHSLVPYGYTLQFWHVLAAARLAFIIVFEHLVFCIKHLISYL 870

Qy      872  VPDIPESVEIKVKREYLLAKQALAENEVLFGTNGTKDEQPKGSELSSHW 920
      :||:|: :   ::|| || : : | :|   | : : |   : |
Db      871  IPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNKAHNEW 919

```

RESULT 8

ADK52114

ID ADK52114 standard; protein; 981 AA.

XX

AC ADK52114;

XX

DT 15-JUN-2007 (revised)

DT 20-MAY-2004 (first entry)

XX

DE Human atopic dermatitis/psoriasis-associated protein #29.
 XX
 KW Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory;
 KW antipsoriatic; rash; BOND_PC; transmembrane protein 16C;
 KW chromosome 11 open reading frame 25;
 KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
 KW transmembrane protein 16C (eight membrane-spanning domains);
 KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
 KW GO16021; GO4185; GO7001.
 XX
 OS Homo sapiens.
 XX
 PN W02004016785-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 06-AUG-2003; 2003WO-JP009999.
 XX
 PR 06-AUG-2002; 2002JP-00229319.
 PR 14-MAY-2003; 2003JP-00136544.
 XX
 PA (GENO-) GENOX RES INC.
 PA (UYJU-) UNIV JUNTENDO.
 XX
 PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
 PI Mitsuishi K;
 XX
 DR WPI; 2004-214514/20.
 DR N-PSDB; ADK52028.
 DR PC:NCBI; gil13899227.
 DR PC:SWISSPROT; Q9BYT9.
 XX
 PT Detecting atopic dermatitis or psoriasis comprises assaying levels of
 PT expression of an indicator gene at a rash site and non-rash site of a
 PT person with atopic dermatitis or psoriasis.
 XX
 PS Example 2; SEQ ID NO 147; 484pp; Japanese.
 XX
 CC The invention relates to detecting atopic dermatitis or psoriasis
 CC comprising assaying the levels of expression of an indicator gene at a
 CC rash site and non-rash site of a person with atopic dermatitis or
 CC psoriasis, comparing these levels with those of a healthy person, and
 CC determining that if the levels of indicators are higher or lower, then
 CC this indicates the disease. Also included are a reagent for detecting
 CC atopic dermatitis or psoriasis, a kit for screening for treatments, a
 CC transgenic non human vertebrate animal models for the diseases, an agent
 CC for inducing the diseases in mice and a DNA chip for assaying for the
 CC indicator genes. The method is used for treatment, detection and animal
 CC models for research of atopic dermatitis and psoriasis. The present

CC sequence is a protein encoded by an indicator gene of the invention.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 981 AA;

Query Match 30.4%; Score 1504; DB 8; Length 981;
 Best Local Similarity 39.4%; Pred. No. 8.1e-145;
 Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Qy	106	KPRIADFLVWVEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQDQDVQDGNT	165
		: : : : : : :	
Db	161	KRRI-DYILVYR-----KTNIPTYDKRNTFEKNLRAEGLMLEKEPA-IASP	203
Qy	166	TVHYALLSASWAVLCYAE DLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
		: : : : : : : : : : : :	
Db	204	DIMFIKIHIPWDLTCKYAE RLNIRMPFRKKCYT DGRSKSMGRMQTYFRRIKDWMQNP	263
Qy	216	LLE--VVPDV-PPEYYSCRFRV NKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
		: : : : : : : : : : : : : :	
Db	264	VLDKSAFPDLEESDCYTGPF SRARIHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271	EKKNLLGIHQLLAEGVLSAAFFLHDGPFKT----PPEGPQAPRLNQRQVLFQHWARWGKW	326
		: : : : : : : :	
Db	323	SK---VGIRKLINNGSYIAAFPPEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327	NKYQLDHHVRRYFGKEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
		: : : : : : : : : :	
Db	376	YKHQPLDLIRLYFGEKIGLYFAWLGWYTGM LIPAAIVGLCVFFYGLFTMNNSQVSVQEI	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS	445
		: : : : : : : : : : : : :	
Db	436	ATEVF-MCPLCDKNCSLQRLNDS CIYAKVTYLF DNGGTVFFAIFMAIWATVLEFVWKRRR	494
Qy	446	ATLAYRWDSCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI	504
		: : : : : : : :	
Db	495	SILTYTWDLIEWEEEEETLRPQFEAKYKMEIVNPFITGKPEPHQPSDDKVTLLVSVSGI	554
Qy	505	VVMVAVVVMCLVSIILYR-AIMAIVVSRSNGNTLLA AWASRIASLTGSV-VNLVFILILSK	562
		: : : : : : : : : : : : : : :	
Db	555	FFMISLVITAVFGVVVYRLV VMEQFASFKNWFIKQYW--QFATSA AAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVN FYSSPVYIAFFKGRFVGYPGNYHT	622
		: : : : : : : :	
Db	613	AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVN LNSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWVQKFLRLSKKRKA	681
		: : : : : : : :	

```

Db      673  LFDNRWLEECHPSGCLIDLCLQMGVIMFLKQIWNFMELGYPLIQNWWSRHKI-----KR 727

Qy      682  GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVE 739
      |  ||  ||:|:  |  ||  |||||  |||||  ||||  ||||  :|
Db      728  GIH-DASIPQWENDWNLPQPMNLHGLMDEYLEMVLQFGFTTIFVAAPLAPLLALLNNIIE 786

Qy      740  IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFFLLAFSSDFLPYAYRW- 798
      ||||  |||  ::||:  ||  ||||  ||  |:  |||:|:|:|  :|:|:|  |  :
Db      787  IRLDAYKFVTQWRRRLPARATDIGIWLGLILEGIGILAVITNAFVIAITSDYIPRFVYEYK 846

Qy      799  -----TRAHDLRGFLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDDGHYSQTY 843
      :  |:|:|  |:|  |  :  |||  :|  ::  |
Db      847  YGPCANHVEPSENCLKGYVNNLSLFFDLSELGMGKSGYCRYRDRYRGPWPSSKPYEFTLQY 906

Qy      844  WNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV 899
      |:|  |||:|:|:|  :  :  |:|:|  :  ::|  ||  :  :  |  :
Db      907  WHILAAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEAE 962

```

RESULT 9

AEN06206

ID AEN06206 standard; protein; 981 AA.

XX

AC AEN06206;

XX

DT 15-JUN-2007 (revised)

DT 22-FEB-2007 (first entry)

XX

DE Human esophageal cancer-associated protein SEQ ID NO 231.

XX

KW diagnostic; metastasis; esophagus tumor; gastrointestinal disease;
 KW neoplasm; cytostatic; cancer; AXL; ZBTB11; TNFRSF14; NSUN5; SPEN; LTBP3;
 KW SYNGR1; SLC13A1; MAP3K12; GLYAT; ZNF659; B4GALT2; POGK; AQP3; CAPG;
 KW SLIT2; BOND_PC; transmembrane protein 16C;
 KW chromosome 11 open reading frame 25;
 KW transmembrane protein 16C [Homo sapiens]; TMEM16C; C11orf25; GENX-3947;
 KW transmembrane protein 16C (eight membrane-spanning domains);
 KW hypothetical protein; hypothetical protein [Homo sapiens]; GO16020;
 KW GO16021; GO4185; GO7001.

XX

OS Homo sapiens.

XX

PN WO2006118308-A1.

XX

PD 09-NOV-2006.

XX

PF 02-MAY-2006; 2006WO-JP309177.

XX

PR 02-MAY-2005; 2005JP-00134530.

PR 13-SEP-2005; 2005JP-00265645.

PR 13-SEP-2005; 2005JP-00265678.

XX

PA (TORA) TORAY IND INC.

PA (KYOU) UNIV KYOTO.

XX

PI Akiyama H, Kozono S, Myomoto A, Nomura O, Nobumasa H, Tanaka Y;

PI Tomoda S, Shimada Y, Tsujimoto G;

XX

DR WPI; 2007-110304/11.

DR PC:NCBI; gi13899227.

DR PC:SWISSPROT; Q9BYT9.

XX

PT Composition for determining occurrence/metastasis of esophageal cancer in
PT subject, comprises an antibody binding to a polypeptide encoded by a
PT polynucleotide having a sequence of genes e.g. AXL, ZBTB11 and TNFRSF14,
PT and/or polynucleotides.

XX

PS Claim 1; SEQ ID NO 231; 142pp; Japanese.

XX

CC This invention describes a novel composition for detecting metastasis of
CC esophageal cancer in a test subject. The composition contains a probe
CC derived from polynucleotides AXL, ZBTB11, TNFRSF14, NSUN5, SPEN, LTBP3,
CC SYNGR1, SLC13A1, MAP3K12, GLYAT, ZNF659, B4GALT2, POGK, AQP3, CAPG,
CC SLIT2, their variants or fragments and an antibody. The invention also
CC claims: a) a kit for detecting, determining or presuming the occurrence
CC or metastasis of esophageal cancer in a test subject; b) a DNA chip for
CC detecting, determining or presuming the occurrence or metastasis of
CC esophageal cancer and c) a method to detect, determine or presume the
CC occurrence or metastasis of esophageal cancer in a test subject by
CC detecting the presence of or amount or expression level of one or more
CC esophagus-cancer related target nucleic acid in a biological sample. The
CC method enables the rapid and convenient detection of occurrence or
CC metastasis of esophageal cancer in test subject with high sensitivity.
CC This sequence represents a protein used in the method of the invention

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 981 AA;

Query Match 30.4%; Score 1504; DB 12; Length 981;
Best Local Similarity 39.4%; Pred. No. 8.1e-145;
Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Qy 106 KPRIADFLVLVVEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQDQDVQDGNT 165
| || ||::||: ::: | || |||| || :::: :
Db 161 KRRI-DYILVYR-----KTNIPIYDKRNTFEKNLRAEGLMLEKEPA-IASP 203

Qy	166	TVHYALLSASVAWLCYYAEDLRKLPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
		: : : :: : : : : : : :	
Db	204	DIMFIKIHIPWDTLCKYAERLNIRMPFRKKCYTDGRSKSMGRMQTYFRRIKDWMAQNPM	263
Qy	216	LLE--VVPDV-PPEYYSCRFRVKNLPRFLGSDNQDTFFTTSTKRHQILFEILAKTPY--GH	270
		: : : : : :: : : : : : : : :	
Db	264	VLDKSAFPDLEESDCYTGPFSSRARIHHFI--INNKDFFFSNATSRIVYHMLERTKYENGI	322
Qy	271	EKKNNLGIHQLLAEGVLSAAFFLHDGPFKT----PPEGPOAPRLNQRQVLFQHWARWGKW	326
		: : : : : : :	
Db	323	SK---VGIRKLINNGSYIAAFPHEGAYKSSQPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327	NKYQLDHVRRYFGEKVALYFAWLGFTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
		: : : : : : : : : : : :	
Db	376	YKHQPLDLIRLYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNSQVQSQEICK	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLEYWKRKS	445
		: : : : : : : : : : : : : : : : :	
Db	436	ATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLFDNNGTVFFAIFMAIWATVLEFWKRRR	494
Qy	446	ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARMLAGSVVI	504
		: : : : :	
Db	495	SILTYTWDLIEWEEEEETLRPQFEAKYKMEIVNPITGKPEHPQSSDKVTRLLVSVSGI	554
Qy	505	VVMVAVVMCLVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSK	562
		::: : ::: : : : : : : : : : : : :	
Db	555	FFMISLVITAVFGVVVYRLVMEQFASFKNFQY--QFATSAAAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLRWEMHRTQTKFEDAFTLKVFIQFVNFYSSPVYIAFFKGRFVGYPGNYHT	622
		::: :::: : : : : : : : :	
Db	613	AYEKIAYLLTNLEYPRTESEWENSFALKMFLQFVNLNSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LFG-VRNEECAAGGLIELAQELLVIMVGQVINNMQEVLIPLKLGWWQKFLRSKKRKA	681
		: : : : : : : : : : : :	
Db	673	LFDRWRLEECHPSGCLIDLCLQMGVIMFLQIWNFMELGYPLIQNWSRHKI-----KR	727
Qy	682	GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFTVFVAACPLAPLALLNNWVE	739
		: : :	
Db	728	GIH-DASIPQWENDNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAPLAPLALLNNIE	786
Qy	740	IRLDARKFVCEYRRPVAERAQDQIGIWFHILAGLTHLAVISNAFFLLAFSSDFLPRAYRW-	798
		: : : : : : : : : :	
Db	787	IRLDAYKFVTQWRRLPARATDIGILEGIGILAVITNAFVIATSDYIPRFVYEYK	846
Qy	799	-----TRAHDLRGLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDDGHSQTY	843
		: : : : : : : : : : : : : : :	
Db	847	YGPCANHVPESENCLKGYVNNLSFFDLSELGMGKSGYCRYRDIRGPPWSSKPYEFTLQY	906
Qy	844	WNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEV	899

|::|| ||||:||||:| | : : |::||: : ::|| || : : | |:

Db 907 WHILAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEAE 962

RESULT 10

AFB77190

ID AFB77190 standard; protein; 1017 AA.

XX

AC AFB77190;

XX

DT 28-JUN-2007 (first entry)

XX

DE Mouse TM-1 (Tmem16a) protein.

XX

KW Cell isolation; stem cell; therapeutic; transgenic animal; screening;

KW tissue regeneration; genitourinary disease; uropathic;

KW intervertebral disk displacement; degeneration; injury; vulnerary;

KW back pain; transmembrane factor-1; Tmem16a.

XX

OS Mus musculus.

XX

PN WO2007027583-A2.

XX

PD 08-MAR-2007.

XX

PF 28-AUG-2006; 2006WO-US033491.

XX

PR 31-AUG-2005; 2005US-0713400P.

XX

PA (UYFL) UNIV FLORIDA RES FOUND INC.

XX

PI Harfe BD, Cohn MJ;

XX

DR WPI; 2007-412931/39.

DR N-PSDB; AFB77189.

XX

PT Isolating sonic hedgehog expressing-cells comprises obtaining a non-human

PT transgenic subject in which a marker gene has been inserted into the

PT subject's genome.

XX

PS Disclosure; SEQ ID NO 2; 96pp; English.

XX

CC The present invention relates to a method of isolating cells in selected
CC tissues co-expressing the sonic hedgehog (Shh) gene and a marker gene.

CC The method involves obtaining a non-human transgenic subject in which a

CC marker gene has been inserted into the subject's genome and isolating

CC Shh/marker gene expressing cells and Shh/marker gene non-expressing cells

CC from the selected tissue. The invention further provides a method of

CC identifying differentially expressed genes (e.g. transmembrane factors TM

CC -1 and TM-2, EST 1437418, Mmu-miR-135a-2 and AP-2 beta) in selected
 CC tissues co-expressing the sonic hedgehog gene and a marker gene. The
 CC invention is useful in tissue engineering, regeneration, reconstruction
 CC and/or repair of tissues and genitourinary system and also in treating
 CC intervertebral disk rupture, degeneration, disease or injury and back
 CC pain. The invention is further useful for generating transgenic animal.
 CC The present sequence is the mouse TM-1 (Tmem16a) protein.

XX

SQ Sequence 1017 AA;

Query Match 30.1%; Score 1489; DB 12; Length 1017;
 Best Local Similarity 37.5%; Pred. No. 3e-143;
 Matches 361; Conservative 170; Mismatches 303; Indels 128; Gaps 29;

```

Qy      26 GLYCRDQHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYG 83
      ||| || : : : || || || : | : | :
Db      109 GLYFRDGRKRVYILVYHHKRASG-----SRTLARRGLQNDMVL-----GTRS 151

Qy      84 STAHASEPGGQQAACRAGSPAKPRIADFLVWEEEDLKLDQRQDQSAARDRTDMHRTWRET 143
      || : : |||| | : | : | | |
Db      152 VRQDQPLPG--KGSPVDAGSPEVP-----MDYHEDD-----KRFRREE 187

Qy      144 FLDNLRAAGLCVDQDQVDGNTTVH---YALLSASWAVLCYYAEDRLKLPLQLPQNQAS 200
      : || ||| : : | : | : : | | || | | : | : | : : :
Db      188 YEGNLEAGLELE---NDEDTKIHGVGVFKIHAPWHVLCREAEFLKLMKPTKKVYHISE 243

Qy      201 NWSAGLLAWLGIPNVLLVVPDVPPEYYSCRFRVNKLPRFLGS-----DNQDTFFT 251
      : ||| | : || : : : | : | : | : | : : | :
Db      244 --TRGLLK--TINSVLQKITDPIQPKVAEHRPQTTKRLSYPFSSREKQHLFDLTDSDFFD 299

Qy      252 STKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLN 311
      | | | : ||| : | : : || || | | | : | | | : |
Db      300 SKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYSAAYPLHDGDY---EGDNV-EFN 353

Qy      312 QRQVLVQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVG 371
      | : | : | | : | : | | : | | | | | | | | | | | : | : | : |
Db      354 DRKLLYEAWASYGVFYKYQPIDLVRKYFGEKVGLYFAWLGAQTMLIPASIVGVIVFLYG 413

Qy      372 CFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM 430
      | | : | : | : : | | | | | : | : | | | | : | | | : | | : |
Db      414 CATVDENIPSMEMCDQRYNIITMCPLCDKTCYSYWKMSACATARASHLFDNPATVFFSVFM 473

Qy      431 ALWAVLLELYWKRKSATLAYRWDCSDYEDTEE---RPRPQFAA-----SAPMTAPNPIT 481
      |||| : | : || | | | : : : || | : : | | : | |
Db      474 ALWAATFMEHWKRRQMRLNYRWDLTGFEETEEAVKDHPRAEYEARVLEKSLRKESRNKET 533

Qy      482 GEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAVVSRSGNTLLAAWA 541
      | : | | | : | : | : : : | : : : : :
Db      534 --DKVKLTWRDRFPAYFTNLVSIIFMIAVTFIIVLGVIIRISTAAALAMNSSPSVRSNI 591

```

Qy 542 SRIASLTGSSVNVLFILILSKIYVSLAHVLRWEMHRTQTKFEDAFTLKVFIFQFVNFYS 601
 : | : : || | | : : | : | : | : : | | : | : : || | :
 Db 592 RVTVTATAVIINLVVILLDEVYGCIAEWLTKEIVPKTEKSFEERLTFKAFLLKFNVSYS 651
 Qy 602 SPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQE 659
 | : || | | | | | | | | : | : | | | | | | | | : | : | : | | | | | : |
 Db 652 PIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFE 711
 Qy 660 VLIPKLKGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCGLFDEYLEMVLQFGFVT 719
 : || | : | : : : || : : : | : | : | | | | : | : | : | | | |
 Db 712 IGIPKMKKFIRYLKLRQSPSDREEYVKRKQRYEVDNFLEPFAGLTPEYMEMIIQFGFVT 771
 Qy 720 IFVAACPLAPLFAALLNNWEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVIS 779
 : || | : | | | | | | | | : | | | | | | | | | | | | : | : | | | |
 Db 772 LFWASFLAPLFAALLNNIIERLDAKKFVTELRRPVAIRAKDIGIWIYNILRGVGLAVII 831
 Qy 780 NAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLARAPSSF-----AAAHN----- 824
 | | : : : | | : | : : : | : | | | | | | | | | | |
 Db 832 NAFVISFTSDFIPRLVLYMYSQNGTMHGFVNHTL---SSFNVSDFQNGTAPNDPLDLG 887
 Qy 825 ---RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIP 876
 : | | : : | : | : | : | | | | | | : : : | : | | | |
 Db 888 YEYQICRYKDYREPPWSEHKYDISKDFWAVLAARLAFVIVFQNLVFMFMSDFVDWVIPDIP 947
 Qy 877 ESVEIKVKREYYL-----AKQALAEENEVLFGTNGTKDEQPKGSELSSHWPFTVP 926
 : : : : : | | | : : : : | : : : : | : | | |
 Db 948 KDISQQIHKEKVMVELFMREEQGGKQQLDWTM-----EKEKPRDVPCNNH-SPTTHP 999
 Qy 927 KA 928
 : |
 Db 1000 EA 1001

RESULT 11

AEG11142

ID AEG11142 standard; protein; 960 AA.

XX

AC AEG11142;

XX

DT 15-JUN-2007 (revised)

DT 20-APR-2006 (first entry)

XX

DE Human transmembrane protein 16A, SEQ ID NO: 7.

XX

KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;

KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;

KW transmembrane protein 16A;

KW transmembrane protein 16A (eight membrane-spanning domains);

KW oral cancer overexpressed 2; membrane protein;
 KW tumor amplified and overexpressed sequence 2;
 KW transmembrane protein 16A [Homo sapiens]; TMEM16A; TAOS2; ORAOV2;
 KW FLJ10261.
 XX
 OS Homo sapiens.
 XX
 PN US2006040292-A1.
 XX
 PD 23-FEB-2006.
 XX
 PF 08-JUL-2005; 2005US-00177894.
 XX
 PR 08-JUL-2004; 2004US-0586676P.
 XX
 PA (WEST/) WEST R B.
 PA (VRIJ/) VAN DE RIJN M.
 XX
 PI West RB, Van De Rijn M;
 XX
 DR WPI; 2006-182760/19.
 DR N-PSDB; AEG11136.
 DR REFSEQ; NP_060513.
 DR PC:NCBI; gi40354210.
 XX
 PT Classifying tumor as gastrointestinal stromal tumor belonging to PDGFRA
 PT positive subclass, involves detecting expression or activity of gene
 PT encoding DOG1 polypeptide in sample.
 XX
 PS Disclosure; SEQ ID NO 7; 177pp; English.
 XX
 CC The present invention relates to three gene markers such as DOG1, KIT and
 CC platelet derived-growth factor receptor alpha (PDGFRA) that are useful in
 CC classifying tumors. These gene markers are useful in the classification
 CC of gastrointestinal stromal tumors (GISTs) and tumors other than GISTs.
 CC The invention also relates to methods providing diagnostic, prognostic
 CC and predicative information based on the classifying step. The invention
 CC is useful for classifying gastrointestinal stromal tumors as belonging to
 CC a PDGFRA positive subclass, KIT negative or PDGFRA negative subclass. The
 CC present sequence is human transmembrane protein 16A (DOG1; TMEM16A). The
 CC DOG1 gene encodes a transmembrane protein of unknown function
 CC (transmembrane protein 16A). The transmembrane protein 16A is encoded by
 CC DOG1 gene that is mapped to 11q13.2 on chromosome 11.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 960 AA;

Query Match 30.1%; Score 1488; DB 11; Length 960;
 Best Local Similarity 37.6%; Pred. No. 3.5e-143;
 Matches 363; Conservative 160; Mismatches 307; Indels 136; Gaps 28;

Qy	26	GLYCRDQAAHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSGY	83
		: : : : :	
Db	52	GLYFRDGRRKVDYILVYHKKRPSG-----NRTLVRVQHS DTP-----SGA	92
Qy	84	STAHASEPGGQQAACRAGSPAKPRIADFLVWVEEDLKLDRQQD SAARDRTDMHRTWRET	143
		: : : : : : :	
Db	93	RSVKQDHP L PGKGASLDAGSGEPP-----MDYHEDD-----KRFREE	130
Qy	144	FLDNLRAAGLCVDVQDVGNTTVH---YALLSASWAVLCYAE DLRLKLPLQELPNQAS	200
		: : : : : : : : : : : : :	
Db	131	YEGNLL EAGLELE----RDEDTKIHG VGFKIHAPWNVLCREAEFLKLMPTKKMYH--I	184
Qy	201	NWSAGLLAWLGIPNVLLVVPDPVPEYYSCR-----FRVNKLPRFLGSDNQD TFF	250
		: : : : : : : : :	
Db	185	NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYFPFSREKQHLFDLSD-KDSFF	241
Qy	251	TSTKRHQILFEILAKTPYGHEKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRL	310
		: : : : : : : : : :	
Db	242	DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY----NGENVEF	295
Qy	311	NQRQVL FQHWARWGKWNKYQPLDHVRRYFGEKV ALYFAWLGFYTGWLLPAAVVGTIVFLV	370
		: : : : : : : : : : : : : :	
Db	296	NDRKLLYE EWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLG VYTQMLIPASIVGIIVFLY	355
Qy	371	GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSFLF	429
		: : : : : : : : : : : :	
Db	356	GCATMDENIPSMEMCDQRHNITMCP LCKTKCSYWKMSACATARASHLFDNPATVFFSVF	415
Qy	430	MALWAVL LLEYWKRSATLAYRWDCSDYEDTEE---RPRPQFAA----SAPMTAPNPI	480
		: : : : : : : : : : : :	
Db	416	MALWAATFMEHWKRKQMRNLNRYWDLTGFE EEEAVKDHPRAEYEARVLEKSLKKE SRNKE	475
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
		: : : : : : : : : : : : : :	
Db	476	T--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPVSRSN	533
Qy	541	ASRIASLTGSVVNLVFI LILSKIYVSLAHVLRWEMHRTQTKEFAFTLKVFI FQVNFY	600
		: : : : : : : : : : :	
Db	534	IRVTVTATAV I INLVII LDEVYGCIARWLTKEI VPKTEKSFEE RLIFKAFLLKFVNSY	593
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQ	658
		: : : : : : : :	
Db	594	TIPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLF	653
Qy	659	EVLIPKLKGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFV	718

```

      |: |||:| : :|: : : :| || | | || |||:|:||||
Db      654 EIGIPKMKKLIRYLKLKQQSPDHEECVKKRKQRYEVDYNLEPFAGLTPEYMEMIIQGFV 713

Qy      719 TIFVAACPLAPLPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVI 778
      |:|||: |||||:||||| :||||:| | | |||||:|:| | : |||
Db      714 TLFVASFPLAPLPLFALLNNIIIEIRLDAKKFVTELRRPVAVRKDIGIWNILRGIGKLAVI 773

Qy      779 SNAFLLAFFSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN----- 824
      |||::|:|:|:| | : : : : | | | | | | | | | | | |
Db      774 INAFVISFTSDFIPRLVLYLYMSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDL 829

Qy      825 ----RTCRYAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDI 875
      : |||: :|: : : | : : | | | |||||:|:| : : |||
Db      830 GYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVFMFMSDFVDWVIPDI 889

Qy      876 PESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----KG 913
      | : : : :| | | | | | | | | | | | | | | | |
Db      890 PKDISQQIHKEKVLMLVLFMREEQDKQQLL--ETWMEKERQKDEPPCNHNTKACPDSLG 947

Qy      914 SELSSH 919
      | ||
Db      948 SPAPSH 953

```

RESULT 12

AEG11146

ID AEG11146 standard; protein; 840 AA.

XX

AC AEG11146;

XX

DT 15-JUN-2007 (revised)

DT 20-APR-2006 (first entry)

XX

DE Human transmembrane protein 16A, SEQ ID NO: 11.

XX

KW Genetic marker; diagnostic; prognosis; gastrointestinal tumor;

KW cytostatic; neoplasm; tumor marker; transmembrane protein 16A; BOND_PC;

KW TMEM16A protein; TMEM16A protein [Homo sapiens].

XX

OS Homo sapiens.

XX

PN US2006040292-A1.

XX

PD 23-FEB-2006.

XX

PF 08-JUL-2005; 2005US-00177894.

XX

PR 08-JUL-2004; 2004US-0586676P.

XX

Qy	302	PEGPQAPRLNQRQVLFFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAA	361
Db	173	--NGENVEFNDRLKLLYEWEARYGVFYKQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPAS	230
Qy	362	VVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDH	420
Db	231	IVGIIVFLYGCATMDENIPSMEMCDQRHNITMCPLCDKTCSYWKMSACATARASHLFDN	290
Qy	421	GGTVFFSLFMALWAVLLEWYWRKKSATLAYRWDCSDYEDTEERPRPQFAA-----SAPMT	475
Db	291	PATVFFSVFMALWAATFMEHWKRKQMLNRYRWDLTGFEEDDHPRAEYEARVLEKSLKKE	350
Qy	476	APNPITGEDEPYFPERSARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNT	535
Db	351	SRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFIVLGVIIYRISMAAALAMNSSP	408
Qy	536	LLAAWASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKEFAFTLKVFIFQ	595
Db	409	SVRSNIRVTVTATAVINLVIIILLDEVYGCARWLTKIEVPKTEKSFEERLIFKAFLLK	468
Qy	596	FVNFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI	654
Db	469	FVNSYTPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCQLSIIIMLGKQLI	528
Qy	655	-NNMQEVLIPKLKGWQKFLRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVL	713
Db	529	QNNLFEIGIPKMKKLIIRYLKLKQQSPPDHEECVKKRQRYEVDYNLEPFAGLTPEYMEMII	588
Qy	714	QGFVTFIFVAACPLAPLAFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLT	773
Db	589	QGFVTFIFVASFPLAPLAFALLNNIIEIRLDAKKFVTELRRPVAVRAKDIGIWINILRGIG	648
Qy	774	HLAVISNAFLAFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN	824
Db	649	KLAVIIDAFAVISFTSDFIPRLVLYLYMSKNGTMHGFVNHTL----SSFNVSDFQNGTAPN	704
Qy	825	-----RTCRYAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDL	870
Db	705	DPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVFMMSDFVDW	764
Qy	871	LVPDIPESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----	911
Db	765	VIPDIPKDISQIHKKEKVLVLMVELFMREEQDKQQLL--ETCMEKERQKDEPPCNHNTKAC	822
Qy	912	---KGSELSSH	919
Db	823	PDSLGSPPASH	833

RESULT 13

ADG48280

ID ADG48280 standard; protein; 1003 AA.

XX

AC ADG48280;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human retina-specific protein - C12orf3variants.

XX

KW human; retina-specific protein; NET01; retinal disease;

KW age related macular degeneration; night blindness; C12orf3variants.

XX

OS Homo sapiens.

XX

PN WO2003068967-A2.

XX

PD 21-AUG-2003.

XX

PF 18-FEB-2003; 2003WO-EP001625.

XX

PR 18-FEB-2002; 2002EP-00003675.

PR 21-FEB-2002; 2002US-0357857P.

XX

PA (LYNK-) LYNKEUS BIO TECH GMBH.

XX

PI Stoehr BH, Weber FHB, Goehring F;

XX

DR WPI; 2003-767334/72.

DR N-PSDB; ADG48279.

XX

PT New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
 PT retinal disease, especially macular degeneration, also for drug screening
 PT and therapy.

XX

PS Claim 18; Fig 14; 199pp; English.

XX

CC The invention comprises the amino acid and coding sequences of a human
 CC retina-specific protein - NET01. The DNA and protein sequences of the
 CC invention are useful in the treatment of retinal diseases, such as
 CC macular degeneration (especially age related) and night blindness. The
 CC present amino acid sequence represents the human retina-specific protein
 CC C12orf3variants.

XX

SQ Sequence 1003 AA;

Query Match 29.6%; Score 1464; DB 7; Length 1003;

Best Local Similarity 37.4%; Pred. No. 1.1e-140;

http://es.ScoreAccessWeb/GetItem.action?AppId=10552...4 083145 us-10-552-515-1.rag&ItemType=4&startByte=0 (38 of 44)10/10/2008 8:48:10 AM

Qy	758	RAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLA--	813
		: : : : : : : : : : : : : :	
Db	796	RTKDIGIWFEDILSGIGKFSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFEVNHLSFF	855
Qy	814	-----RAPSSFAAAHNRTCRYAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEH	859
		: : : :: : : : : : : : : : :	
Db	856	NVSQLKEGTQPENSQFDQEVQFCRFKDYREPPWAPNPYEFQYWFILSARLAFVIFQN	915
Qy	860	VVFSVGRLLDLLVPDIPESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKG	913
		: : : : : : : : : : : : : : :	
Db	916	LVMFLSVLVDWMIPDIPTDISDQIKKEKSLLVDFFLKE----EHEKCLKLMDEPALRSPGG	971
Qy	914	SELSSHWPFTVPKA-SQL	931
		: :	
Db	972	GDRSRRAAASPAGSOSOL	990

RESULT 14

AEH82071

ID AEH82071 standard; protein; 913 AA.

XX

AC AEH82071;

XX

DT 15-JUN-2007 (revised)

DT 13-JUL-2006 (first entry)

XX

DE Human gnathodiaphyseal dysplasia protein, GDD1.

XX

KW Osteopathic; Gene therapy; bone disease; bone injury; bone resorption;

KW gnathodiaphyseal dysplasia; GDD1; BOND_PC; transmembrane protein 16E;

KW integral membrane protein GDD1; transmembrane protein 16E [Homo sapiens];

KW TMEM16E; GDD1; integral membrane protein GDD1 [Homo sapiens]; G05783;

KW GO16020; GO16021.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT Inhibitory-site 356

```
FT          /note= "Missense mutations in the coding sequence can
```

FT lead to substitution of this residue with either Arg or

FT Gly"

XX

PN JP2006121961-A.

XX

PD 18-MAY-2006.

XX

PF 28-OCT-2004; 2004JP-00313511.

XX

PR 28-OCT-2004; 2004JP-00313511.
 XX
 PA (UYTO-) UNIV TOKUSHIMA NAT UNIV CORP.
 XX
 PI Itakura M, Tsutsumi S, Kamata N, Inoue H;
 XX
 DR WPI; 2006-367194/38.
 DR N-PSDB; AEH82070.
 DR PC:NCBI; gi47106048.
 DR PC:SWISSPROT; Q75V66.
 XX
 PT Novel gnathodiaphyseal dysplasia DNA, useful as diagnostic agent for bone
 PT disease such as gnathodiaphyseal dysplasia, bone deficiency or bone-
 PT resorption property disease.
 XX
 PS Claim 9; SEQ ID NO 2; 11pp; Japanese.
 XX
 CC The present invention relates to a human gnathodiaphyseal dysplasia (GDD)
 CC coding sequence (GDD1; AEH82070) and encoded protein (AEH82071). GDD1 is
 CC useful as a bone disease diagnostic agent, where the bone disease is GDD,
 CC bone deficiency and/or bone-resorption property disease, where the GDD
 CC disease causes hardening of bone, susceptibility to fracture, cement bone
 CC pathology of a lower jaw bone, etc. GDD1 is also useful in bone formation
 CC regeneration, hard tissue reconstruction, etc., and in research
 CC application.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 913 AA;

Query Match 29.4%; Score 1455; DB 11; Length 913;
 Best Local Similarity 38.6%; Pred. No. 8.4e-140;
 Matches 325; Conservative 154; Mismatches 276; Indels 86; Gaps 22;

Qy 108 RIADFVLVWEEDLKLDQQDSAARDRTDMHRTWRETFLDNLRAAGL---CVDQQDVQDGN 164
 | ||| : :| | : : | : | || | : : | : |
 Db 78 RQIDFVLSYVDDVKD-----AELKAERRKEFETNLRKGTGLELEIEDKRDSEdGR 127

Qy 165 TTVHYALLSASWAVLCYYAEDLRKLPLQE--LPNQASNWSAGLLAWLGIPNVLLVVPD 222
 | : : | | || || | :| : : | : | : : | : | : |
 Db 128 T--YFVKIHAPWEVLVTYAEVLGIKMPIKESDIPRPKHTPISYVLGPVRLP--LSVKYPH 183

Qy 223 VPPEYYSCRFRVKNLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHEK-KNLLGIHQ 281
 ||| : : | : : || | | || | : : : : || : : | | | : |
 Db 184 --PEYFTAQFSRHRQELFLIED-QATFFPSSSRNRIVYYILSRCPFIEDGKKRFGIERL 240

Qy 282 LAEGVLSAAFLPHDGPFKTPPEGPQAPRLNQRLVLFQHWARWGKWNKYQPLDHVRRYFGE 341
 | :| :||| | : | | | :| | :| : : | ||| : :| :

Db	241	LNSNTYSSAYPLHDGQYWKPEPPNP--TNERYTLHQNWARFSYFYKEQPLDLIKNYGGE	298
Qy	342	KVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSFEMCPLCLD	399
Db	299	KIGIYFVFLGFYTEMFLFAAVVGLACFIYGLLSMEHNTSSTEICDPEIGGQMIMCPLCDQ	358
Qy	400	-CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYE	458
Db	359	VCDYWRLNSTCLASKFSLFDNESTVFFAIFMGIWVTLFLEFWKQQRARLEYEWDLVDFE	418
Qy	459	DTEE--RRRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLV	516
Db	419	EEQQQLQLRPEFEAMCKHRKLNNAVTKEMEPLYTRIPWYFLSGATVTLWMSLVVTSMV	478
Qy	517	SIILYRAIMAIIVSRSGNTLLAAWASRI-----ASLTGSVNVNLFVIL	558
Db	479	AVIVYRL-----SVFATFASFMESDASLKQVKSFLTPQITTSLTGSCLNFIVIL	527
Qy	559	ILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPG	618
Db	528	ILNFFYEKISAWITKMEIPRTYQYESSLTLKMFLFQFVNFYSSCFYVAFKKGKFGVYPG	587
Qy	619	NYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFLRLSK	677
Db	588	KYTYLFNEWRSEECDPGGCLIELTTQLTIIMTGKQIFGNIKEAIYPLALNWW-----R	640
Qy	678	KRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLALLN	735
Db	641	RRKARTNSEKLYSRWEQDHDLESFGPLGLFYEYLETVTQFGFVTLFVASFPLAPLLALIN	700
Qy	736	NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAY	795
Db	701	NIVEIRVDAWKLTQYQRTVASKAHSIGVWQDILYGMVLSVATNAFIVAFSTSDIIPRLV	760
Qy	796	YRW----TRAHDRLRGFLN----FTLARAPSSFAAAHNR---TCRYRAFR---DDGDHY-	839
Db	761	YYYAYSTNATQPMGTGYNNLSVFLIADFPNHTAPSEKRDFTICRYRDYRYPDPDENKYF	820
Qy	840	-SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAE	898
Db	821	HNMQFVHWVLAAKMTFIIIVMEHVFLVKFLLAWMIPDPVPRDVERIKREKLMTIKILHDFE	880
Qy	899	V 899	
Db	881	L 881	

ID ABB62812 standard; protein; 1219 AA.
 XX
 AC ABB62812;
 XX
 DT 15-JUN-2007 (revised)
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15228.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; BOND_PC; CG6938-PA; CG6938-PA [Drosophila melanogaster];
 KW CG6938.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL06915.
 DR PC:NCBI; gi24663059.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 15228; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 1219 AA;

Query Match 29.2%; Score 1445; DB 4; Length 1219;
 Best Local Similarity 35.6%; Pred. No. 1.4e-138;
 Matches 342; Conservative 165; Mismatches 332; Indels 122; Gaps 27;

Qy 35 AERWAMTSETSSGSHCARSRML-----RRRAQBEDSTVLIDVSPPEAEKRGSY 82
 |:| :| || |:| |:| :| |:| |||
 Db 249 ADRVNQSYEVMESSH---SNVLPDQFGYRQLIPTERKASDTASSV-----SGSY 294

Qy 83 GSTAHASEP---GGQQAACRAGSPAKP-----RIADFLVW-EEDLKLDRQ 125
 : ||: ||: | : | || | ||| : :
 Db 295 YGSRKASKSNSLGGESGDERRVSKQDREGLDPESLMFRDGRKVDMLAWEEEDLGVMT 354

Qy 126 QDAAARDRTDMHRTWRETFDLNLRAGLCVDQDD-VQDGNTHVYALLSASWAVLCYYAE 184
 :: || |:|:| || |:| | | : : | : ||
 Db 355 AEAKRRDN-----RRSFMENLIKEGLEVELEDKSSQSFNEKTFFLKIHLPRWLETRLAE 407

Qy 185 DLRLKLP-----LQELPNQASNWSAGLLAWLGIPNVLLVVPDVP 225
 : ||| |: : | | : : |||
 Db 408 VMNLKLPVKRFITISVKPSWDEENVLRNMQYWKDVWQR-LTKKIQLDQTLE---GET 462

Qy 226 EYYSRCFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEG 285
 : : | :|: | : | ||| :| : : :| :|: : : | :|: :|
 Db 463 TFKAATANGNPEEQFIVKD-RATAFTSAQSRSLVMQVLIRTPFDES DRS--GIRRLMNDG 519

Qy 286 VLSAAFPLHDGPFKTPPEGPOAPRLN-QRQVLFQHWARWGKNKYQPLDHVRRYFGEKVA 344
 |||:| : : | : : : |:|:| || :| | || | |:|:|:|:|
 Db 520 TYLGCFPLHEGRY----DRPHSSGISLDRRVLYQTWAHP SQWYKQPLCLVRKYFGDKIA 575

Qy 345 LYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFS--IPTQELCG--SKDSFEMCPLC-LD 399
 || | |||| | : | |||| |: | : |: |:| : : : |||
 Db 576 LYFCWLGFYTEMLVYPVAVGTLCFIYGLATLESDNTSPSKEICNEYGTGNITLCPLCDKA 635

Qy 400 CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYED 459
 | : || :| : : |||: |||:|:| || || ||| : | : | : |
 Db 636 CSYQRLSESCLSRLTYLFDNPSTVFFAIFMSFWATTFLELWKRKQSVLVWEWDLHNV-D 694

Qy 460 TEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSI 519
 :| ||:| :| ||:| ||| |:| : : :|:|:| : : |
 Db 695 MDEENRPEFETNATTFRMNPVTREKEPYMSTWNR SIRFVITGSVLFMISVVL SAVLGTI 754

Qy 520 LYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFIILSKIYVSLAHLVTRWEMHRT 579
 ||| : |: | : | |:| :|:| |:|:|:| :| || | ||
 Db 755 LYRITLVSVIYGGGGFFVKEHAKLFTSVTAALINLVVIMILTRIYHRMAIKLTNLENPT 814

